

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANT: Melton, Douglas A.  
Hemmati-Brivanlou, Ali

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(ii) TITLE OF INVENTION: Method of Inducing and Maintaining  
Neuronal Cells

(iii) NUMBER OF SEQUENCES: 2

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD  
(B) STREET: 60 State Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
20 (F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: ASCII(TEXT)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
30 (B) FILING DATE: 09-MAR-1995  
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Vincent, Matthew P.  
35 (B) REGISTRATION NUMBER: 36,709  
(C) REFERENCE/DOCKET NUMBER: HUI-009

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(ix) TELECOMMUNICATION INFORMATION:

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(A) TELEPHONE: (617) 227-7400  
(B) TELEFAX: (617) 227-5941

## (2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

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(A) NAME/KEY: CDS  
(B) LOCATION: 108..1067

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGGCCGCC CCCCCCCC GT CATTCAATAG AGTCCGGACT TGTGCCTGGT CCATTATCCC

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ATCTCTCTCC ACTTGAGACT CTGCTCGTCC CACTCCCAGC ACTGAGG ATG TTA AAT

Met Leu Asn

116

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	GAA AGG ATC CAG CCG GGC ATG ATT TTC CTC CTG ACT GTC TCC CTG TGC Glu Arg Ile Gln Pro Gly Met Ile Phe Leu Leu Thr Val Ser Leu Cys 5 10 15	164
5	CAT TTC ATG GAA TAT CGC GCA GTC CAA GCT GGG AAT TGC TGG CTG CAG His Phe Met Glu Tyr Arg Ala Val Gln Ala Gly Asn Cys Trp Leu Gln 20 25 30 35	212
10	CAG TCG AAG AAT GGC CGA TGT CAG GTT CTG TAC AGG ACA GAA CTG AGC Gln Ser Lys Asn Gly Arg Cys Gln Val Leu Tyr Arg Thr Glu Leu Ser 40 45 50	260
15	AAA GAG GAA TGC TGC AAG ACT GGC AGA CTG GGC ACC TCA TGG ACA GAA Lys Glu Glu Cys Cys Lys Thr Gly Arg Leu Gly Thr Ser Trp Thr Glu 55 60 65	308
20	GAA GAT GTA CCC AAC AGC ACC CTC TTC AAA TGG ATG ATA TTT CAT GGA Glu Asp Val Pro Asn Ser Thr Leu Phe Lys Trp Met Ile Phe His Gly 70 75 80	356
25	GGG GCC CCA CAT TGC ATC CCC TGC AAA GAA ACA TGT GAG AAC GTA GAC Gly Ala Pro His Cys Ile Pro Cys Lys Glu Thr Cys Glu Asn Val Asp 85 90 95	404
30	TGT GGC CCT GGG AAG AAA TGT AAA ATG AAC AAG AAG AAC AAG CCG AGG Cys Gly Pro Gly Lys Lys Cys Lys Met Asn Lys Lys Asn Lys Pro Arg 100 105 110 115	452
35	TGT GTC TGC GCT CCG GAT TGT TCC AAC ATT ACT TGG AAA GGT TCA GTG Cys Val Cys Ala Pro Asp Cys Ser Asn Ile Thr Trp Lys Gly Ser Val 120 125 130	500
40	TGC GGA ATT GAT GGC AAA ACC TAT AAG GAT GAG TGC GCT TTG CTC AAA Cys Gly Ile Asp Gly Lys Thr Tyr Lys Asp Glu Cys Ala Leu Leu Lys 135 140 145	548
45	GCC AAA TGT AAA GGG GTC CCG GAG CTG GAT GTG CAG TAC CAA GGA AAA Ala Lys Cys Lys Gly Val Pro Glu Leu Asp Val Gln Tyr Gln Gly Lys 150 155 160	596
50	TGC AAA AAG ACT TGC AGG GAC GTG CTG TGT CCA GGG AGC TCC TCG TGT Cys Lys Lys Thr Cys Arg Asp Val Leu Cys Pro Gly Ser Ser Ser Cys 165 170 175	644
55	GTC GTG GAT CAG ACC AAT AAC GCC TAC TGT GTG ACA TGT AAT CGG ATT Val Val Asp Gln Thr Asn Asn Ala Tyr Cys Val Thr Cys Asn Arg Ile 180 185 190 195	692
60	TGC CCG GAG CCT ACC TCC CCT GAC CAA TAT CTG TGT GGG AAT GAT GGA Cys Pro Glu Pro Thr Ser Pro Asp Gln Tyr Leu Cys Gly Asn Asp Gly 200 205 210	740
65	ATA ACC TAT GGA AGT GCG TGC CAC CTG AGG AAG GCT ACC TGC CTG CTG Ile Thr Tyr Gly Ser Ala Cys His Leu Arg Lys Ala Thr Cys Leu Leu 215 220 225	788
70	GGC AGA TCC ATT GGA TTA GCC TAC GAG GGG AAA TGC ATA AAA GCC AAG Gly Arg Ser Ile Gly Leu Ala Tyr Glu Gly Lys Cys Ile Lys Ala Lys 230 235 240	836
75	TCT TGT GAA GAT ATT CAG TGC AGC GCT GGA AAG AAA TGC CTG TGG GAC Ser Cys Glu Asp Ile Gln Cys Ser Ala Gly Lys Lys Cys Leu Trp Asp 245 250 255	884
80	AGT AGA GTG GGT AGA GGT CGC TGT GCG CTG TGC GAT GAT CTG TGC GGA Ser Arg Val Gly Arg Gly Cys Ala Leu Cys Asp Asp Leu Cys Gly	932

260	265	270	275		
GAG AGC AAG TCA GAC GAT ACA GTG TGC GCC AGC GAC AAC ACG ACT TAC				980	
Glu Ser Lys Ser Asp Asp Thr Val Cys Ala Ser Asp Asn Thr Thr Tyr					
5	280	285	290		
CCG AGC GAG TGC GCC ATG AAA CAG GCA GCC TGC TCC ACG GGG ATT CTT				1028	
Pro Ser Glu Cys Ala Met Lys Gln Ala Ala Cys Ser Thr Gly Ile Leu					
	295	300	305		
10	TTG GAA GTG AAA CAC AGT GGA TCT TGC AAC TGT AAG TGAATTACCG				1074
Leu Glu Val Lys His Ser Gly Ser Cys Asn Cys Lys					
	310	315	320		
15	CAACGCAGAG TAAGATTCT AAAGGCAACC CCTCGGTAAAT GAAGACTTTA AAGCAGCAAA				1134
ATACTTTTTT TTTTTTTTT TCCTTTTTT CTAAGGGAAT TCAG				1178	

## 20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:					
(A) LENGTH: 319 amino acids					
(B) TYPE: amino acid					
25	(D) TOPOLOGY: linear				
(ii) MOLECULE TYPE: protein					
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:					
30	Met Leu Asn Glu Arg Ile Gln Pro Gly Met Ile Phe Leu Leu Thr Val				
	1	5	10	15	
35	Ser Leu Cys His Phe Met Glu Tyr Arg Ala Val Gln Ala Gly Asn Cys				
	20	25	30		
40	Trp Leu Gln Gln Ser Lys Asn Gly Arg Cys Gln Val Leu Tyr Arg Thr				
	35	40	45		
45	Glu Leu Ser Lys Glu Glu Cys Cys Lys Thr Gly Arg Leu Gly Thr Ser				
	50	55	60		
50	Trp Thr Glu Glu Asp Val Pro Asn Ser Thr Leu Phe Lys Trp Met Ile				
	65	70	75	80	
55	Phe His Gly Gly Ala Pro His Cys Ile Pro Cys Lys Glu Thr Cys Glu				
	85	90	95		
60	Asn Val Asp Cys Gly Pro Gly Lys Lys Cys Lys Met Asn Lys Lys Asn				
	100	105	110		
65	Lys Pro Arg Cys Val Cys Ala Pro Asp Cys Ser Asn Ile Thr Trp Lys				
	115	120	125		
70	Gly Ser Val Cys Gly Ile Asp Gly Lys Thr Tyr Lys Asp Glu Cys Ala				
	130	135	140		
75	Leu Leu Lys Ala Lys Cys Lys Gly Val Pro Glu Leu Asp Val Gln Tyr				
	145	150	155	160	
80	Gln Gly Lys Cys Lys Lys Thr Cys Arg Asp Val Leu Cys Pro Gly Ser				
	165	170	175		
85	Ser Ser Cys Val Val Asp Gln Thr Asn Asn Ala Tyr Cys Val Thr Cys				
	180	185	190		

Asn Arg Ile Cys Pro Glu Pro Thr Ser Pro Asp Gln Tyr Leu Cys Gly  
195 200 205

5 Asn Asp Gly Ile Thr Tyr Gly Ser Ala Cys His Leu Arg Lys Ala Thr  
210 215 220

Cys Leu Leu Gly Arg Ser Ile Gly Leu Ala Tyr Glu Gly Lys Cys Ile  
225 230 235 240

10 Lys Ala Lys Ser Cys Glu Asp Ile Gln Cys Ser Ala Gly Lys Lys Cys  
245 250 255

Leu Trp Asp Ser Arg Val Gly Arg Gly Arg Cys Ala Leu Cys Asp Asp  
260 265 270

15 Leu Cys Gly Glu Ser Lys Ser Asp Asp Thr Val Cys Ala Ser Asp Asn  
275 280 285

Thr Thr Tyr Pro Ser Glu Cys Ala Met Lys Gln Ala Ala Cys Ser Thr  
290 295 300

Gly Ile Leu Leu Glu Val Lys His Ser Gly Ser Cys Asn Cys Lys  
305 310 315